

SEQUENCE LISTING

<110> E. I. duPont de Nemours and Company, Inc.
Suh, Wonchul
Rouviere, Pierre
Cheng, Qiong

<120> Increasing Carotenoid Production in Bacteria Via Chromosomal Integration

<130> CL2027 US NA

<150> US 60/434618
<151> 2002-12-19

<160> 66

<170> PatentIn version 3.2

<210> 1
<211> 912
<212> DNA
<213> Rana

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<221> misc_feature
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<223> ttg alternative start codon used to encode methionine
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<213> *Pantoea stewartii*

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35 40 45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala
50 55 60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65 70 75 80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
85 90 95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
100 105 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
115 120 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
130 135 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145 150 155 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
165 170 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
180 185 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
195 200 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
210 215 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225 230 235 240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
245 250 255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
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| Arg | Glu | Lys | Leu | His | His | Cys | Phe | Ser | Pro | Leu | Ala | Gln | Ile | Ser | Gln | |
| 195 | | | | | | | 200 | | | | | 205 | | | | |
| ttg | atc | ccc | gaa | ctg | gat | ttt | ccc | cgc | aaa | gcg | ctg | cca | gac | tgc | ttt | 672 |
| Leu | Ile | Pro | Glu | Leu | Asp | Phe | Pro | Arg | Lys | Ala | Leu | Pro | Asp | Cys | Phe | |
| 210 | | | | | | 215 | | | | | 220 | | | | | |
| cat | gcf | gtt | gga | ccg | tta | cgf | caa | ccc | cag | ggg | acg | ccg | ggg | tca | tca | 720 |
| His | Ala | Val | Gly | Pro | Leu | Arg | Gln | Pro | Gln | Gly | Thr | Pro | Gly | Ser | Ser | |
| 225 | | | | | | 230 | | | | 235 | | | | | 240 | |
| act | tct | tat | ttt | ccg | tcc | ccg | gac | aaa | ccc | cgt | att | ttt | gcc | tcg | ctg | 768 |
| Thr | Ser | Tyr | Phe | Pro | Ser | Pro | Asp | Lys | Pro | Arg | Ile | Phe | Ala | Ser | Leu | |
| 245 | | | | | | 250 | | | | | 255 | | | | | |
| ggc | acc | ctg | cag | gga | cat | cgt | tat | ggc | ctg | ttc | agg | acc | atc | gcc | aaa | 816 |
| Gly | Thr | Leu | Gln | Gly | His | Arg | Tyr | Gly | Leu | Phe | Arg | Thr | Ile | Ala | Lys | |
| 260 | | | | | | 265 | | | | | 270 | | | | | |
| gcc | tgc | gaa | gag | gtg | gat | gcf | cag | tta | ctg | ttg | gca | cac | tgt | ggc | ggc | 864 |
| Ala | Cys | Glu | Glu | Val | Asp | Ala | Gln | Leu | Leu | Leu | Ala | His | Cys | Gly | Gly | |
| 275 | | | | | | 280 | | | | | 285 | | | | | |
| ctc | tca | gcc | acg | cag | gca | ggt | gaa | ctg | gcc | cgf | ggg | gac | att | cag | | 912 |
| Leu | Ser | Ala | Thr | Gln | Ala | Gly | Glu | Leu | Ala | Arg | Gly | Gly | Asp | Ile | Gln | |
| 290 | | | | | | 295 | | | | | 300 | | | | | |
| gtt | gtg | gat | ttt | gcc | gat | caa | tcc | gca | gca | ctt | tca | cag | gca | cag | ttg | 960 |
| Val | Val | Asp | Phe | Ala | Asp | Gln | Ser | Ala | Ala | Leu | Ser | Gln | Ala | Gln | Leu | |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 | |
| aca | atc | aca | cat | ggt | ggg | atg | aat | acg | gta | ctg | gac | gct | att | gct | tcc | 1008 |
| Thr | Ile | Thr | His | Gly | Gly | Met | Asn | Thr | Val | Leu | Asp | Ala | Ile | Ala | Ser | |
| 325 | | | | | | 330 | | | | | | 335 | | | | |
| cgc | aca | ccg | cta | ctg | gcf | ctg | ccg | ctg | gca | ttt | gat | caa | cct | ggc | gtg | 1056 |
| Arg | Thr | Pro | Leu | Leu | Ala | Leu | Pro | Leu | Ala | Phe | Asp | Gln | Pro | Gly | Val | |
| 340 | | | | | | 345 | | | | | | 350 | | | | |
| gca | tca | cga | att | gtt | tat | cat | gga | atc | ggc | aag | cgt | gca | tct | cgg | ttt | 1104 |
| Ala | Ser | Arg | Ile | Val | Tyr | His | Gly | Ile | Gly | Lys | Arg | Ala | Ser | Arg | Phe | |
| 355 | | | | | | 360 | | | | | 365 | | | | | |
| act | acc | agc | cat | gcf | ctg | gcf | cgg | cag | att | cga | tcg | ctg | ctg | act | aac | 1152 |
| Thr | Thr | Ser | His | Ala | Leu | Ala | Arg | Gln | Ile | Arg | Ser | Leu | Leu | Thr | Asn | |
| 370 | | | | | | 375 | | | | | 380 | | | | | |
| acc | gat | tac | ccg | cag | cgt | atg | aca | aaa | att | cag | gcc | gca | ttg | cgt | ctg | 1200 |
| Thr | Asp | Tyr | Pro | Gln | Arg | Met | Thr | Lys | Ile | Gln | Ala | Ala | Leu | Arg | Leu | |
| 385 | | | | | | 390 | | | | | 395 | | | | 400 | |
| gca | ggc | ggc | aca | cca | gcc | gcc | gca | gat | att | gtt | gaa | cag | gcf | atg | cgg | 1248 |
| Ala | Gly | Gly | Thr | Pro | Ala | Ala | Ala | Asp | Ile | Val | Glu | Gln | Ala | Met | Arg | |
| 405 | | | | | | 410 | | | | | | 415 | | | | |
| acc | tgt | cag | cca | gta | ctc | agt | ggg | cag | gat | att | gca | acc | gca | cta | tga | 1296 |
| Thr | Cys | Gln | Pro | Val | Leu | Ser | Gly | Gln | Asp | Tyr | Ala | Thr | Ala | Leu | | |
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<212> PRT

<213> Pantoea stewartii

<400> 4

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35 40 45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
50 55 60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65 70 75 80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
85 90 95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
100 105 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
115 120 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
130 135 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145 150 155 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
165 170 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
180 185 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
195 200 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
210 215 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225 230 235 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
245 250 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
260 265 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
290 295 300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305 310 315 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
325 330 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
340 345 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
355 360 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
370 375 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385 390 395 400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
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ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc 96
Gly Leu Ile Ala Leu Arg Leu Gln Gln His Pro Asp Met Arg Ile
20 25 30

ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc 144
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
35 40 45

ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg 192
Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
50 55 60

ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc 240
Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65 70 75 80

cgt cgc cat gtg aac agt ggc tac tac tgc gtg acc tcc cgg cat ttc 288

| Arg | Arg | His | Val | Asn | Ser | Gly | Tyr | Tyr | Cys | Val | Thr | Ser | Arg | His | Phe | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| gcc | ggg | ata | ctc | cgg | caa | cag | ttt | gga | caa | cat | tta | tgg | ctg | cat | acc | 336 |
| Ala | Gly | Ile | Leu | Arg | Gln | Gln | Phe | Gly | Gln | His | Leu | Trp | Leu | His | Thr | |
| 100 | | | | | | | | 105 | | | | | 110 | | | |
| gcg | gtt | tca | gcc | gtt | cat | gct | gaa | tcg | gtc | cag | tta | gcg | gat | ggc | cg | 384 |
| Ala | Val | Ser | Ala | Val | His | Ala | Glu | Ser | Val | Gln | Leu | Ala | Asp | Gly | Arg | |
| 115 | | | | | | | 120 | | | | | 125 | | | | |
| att | att | cat | gcc | agt | aca | gtg | atc | gac | gga | cgg | ggt | tac | acg | cct | gat | 432 |
| Ile | Ile | His | Ala | Ser | Thr | Val | Ile | Asp | Gly | Arg | Gly | Tyr | Thr | Pro | Asp | |
| 130 | | | | | | | 135 | | | | 140 | | | | | |
| tct | gca | cta | cgc | gta | gga | ttc | cag | gca | ttt | atc | ggt | cag | gag | tgg | caa | 480 |
| Ser | Ala | Leu | Arg | Val | Gly | Phe | Gln | Ala | Phe | Ile | Gly | Gln | Glu | Trp | Gln | |
| 145 | | | | | | | 150 | | | | 155 | | | | 160 | |
| ctg | agc | gcf | ccg | cat | ggt | tta | tcg | tca | ccg | att | atc | atg | gat | gcf | acg | 528 |
| Leu | Ser | Ala | Pro | His | Gly | Leu | Ser | Ser | Pro | Ile | Ile | Met | Asp | Ala | Thr | |
| 165 | | | | | | | 170 | | | | | | | 175 | | |
| gtc | gat | cag | caa | aat | ggc | tac | cg | ttt | gtt | tat | acc | ctg | ccg | ctt | tcc | 576 |
| Val | Asp | Gln | Gln | Asn | Gly | Tyr | Arg | Phe | Val | Tyr | Thr | Leu | Pro | Leu | Ser | |
| 180 | | | | | | | 185 | | | | | 190 | | | | |
| gca | acc | gca | ctg | ctg | atc | gaa | gac | aca | cac | tac | att | gac | aag | gct | aat | 624 |
| Ala | Thr | Ala | Leu | Leu | Ile | Glu | Asp | Thr | His | Tyr | Ile | Asp | Lys | Ala | Asn | |
| 195 | | | | | | | 200 | | | | | 205 | | | | |
| ctt | cag | gcc | gaa | cgg | cg | cgt | cag | aac | att | cg | gat | tat | gct | gcf | cga | 672 |
| Leu | Gln | Ala | Glu | Arg | Ala | Arg | Gln | Asn | Ile | Arg | Asp | Tyr | Ala | Ala | Arg | |
| 210 | | | | | | | 215 | | | | | 220 | | | | |
| cag | gg | tgg | ccg | tta | cag | acg | ttg | ctg | cg | gaa | gaa | cag | gg | gca | ttg | 720 |
| Gln | Gly | Trp | Pro | Leu | Gln | Thr | Leu | Leu | Arg | Glu | Glu | Gln | Gly | Ala | Leu | |
| 225 | | | | | | | 230 | | | | 235 | | | | 240 | |
| ccc | att | acg | tta | acg | ggc | gat | aat | cgt | cag | ttt | tgg | caa | cag | caa | ccg | 768 |
| Pro | Ile | Thr | Leu | Thr | Gly | Asp | Asn | Arg | Gln | Phe | Trp | Gln | Gln | Gln | Pro | |
| 245 | | | | | | | 250 | | | | | | | 255 | | |
| caa | gcc | tgt | agc | gga | tta | cgc | gcc | ggg | ctg | ttt | cat | ccg | aca | acc | ggc | 816 |
| Gln | Ala | Cys | Ser | Gly | Leu | Arg | Ala | Gly | Leu | Phe | His | Pro | Thr | Thr | Gly | |
| 260 | | | | | | | 265 | | | | | 270 | | | | |
| tac | tcc | cta | ccg | ctc | g | gt | g | ctg | gcc | gat | cgt | ctc | agc | g | ctg | 864 |
| Tyr | Ser | Leu | Pro | Leu | Ala | Val | Ala | Leu | Ala | Asp | Arg | Leu | Ser | Ala | Leu | |
| 275 | | | | | | | 280 | | | | | 285 | | | | |
| gat | gt | ttt | acc | tct | tcc | tct | gtt | cac | cag | acg | att | gct | cac | ttt | gcc | 912 |
| Asp | Val | Phe | Thr | Ser | Ser | Ser | Val | His | Gln | Thr | Ile | Ala | His | Phe | Ala | |
| 290 | | | | | | | 295 | | | | | 300 | | | | |
| cag | caa | cgt | tgg | cag | caa | cag | ggg | ttt | ttc | cg | atg | ctg | aat | cg | atg | 960 |
| Gln | Gln | Arg | Trp | Gln | Gln | Gly | Phe | Phe | Arg | Arg | Met | Leu | Asn | Arg | Met | |
| 305 | | | | | | | 310 | | | | 315 | | | | 320 | |
| ttg | ttt | tta | gcc | gga | ccg | gcc | gag | tca | cgc | tgg | cgt | gtg | atg | cag | cgt | 1008 |
| Leu | Phe | Leu | Ala | Gly | Pro | Ala | Glu | Ser | Arg | Trp | Arg | Val | Met | Gln | Arg | |
| 325 | | | | | | | 330 | | | | | | | 335 | | |
| tcc | tat | ggc | tta | ccc | gag | gat | ttg | att | gcc | cgc | ttt | tat | g | g | aaa | 1056 |
| Phe | Tyr | Gly | Leu | Pro | Glu | Asp | Leu | Ile | Ala | Arg | Phe | Tyr | Ala | Gly | Lys | |
| 340 | | | | | | | 345 | | | | | | | 350 | | |
| ctc | acc | gt | acc | gat | cg | ct | cg | att | ctg | agc | ggc | aag | ccg | ccc | gtt | 1104 |
| Leu | Thr | Val | Thr | Asp | Arg | Leu | Arg | Ile | Leu | Ser | Gly | Lys | Pro | Pro | Val | |

355

360

365

ccc gtt ttc gcg gca ttg cag gca att atg acg act cat cgt tga 1149
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<213> *Pantoea stewartii*

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Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
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Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
 50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
 65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
 85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
 100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
 115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
 130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
 145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
 165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
 180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
 195 200 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
 210 215 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225 230 235 240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
245 250 255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
260 265 270

Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
275 280 285

Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
290 295 300

Gln Gln Arg Trp Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305 310 315 320

Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
325 330 335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
340 345 350

Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
355 360 365

Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
370 375 380

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<213> Pantoea stewartii

<220>
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gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
20 25 30 96

cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
35 40 45 144

act ttt gat gca ggc cct acc gtt atc acc gat ccc agc gcg att gaa
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
50 55 60 192

gaa ctg ttt gct ctg gcc ggt aaa cag ctt aag gat tac gtc gag ctg
Page 9 240

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Glu | Leu | Phe | Ala | Leu | Ala | Gly | Lys | Gln | Leu | Lys | Asp | Tyr | Val | Glu | Leu | |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 | |
| ttg | ccg | gtc | acg | ccg | ttt | tat | cgc | ctg | tgc | tgg | gag | tcc | ggc | aag | gtc | 288 |
| Leu | Pro | Val | Thr | Pro | Phe | Tyr | Arg | Leu | Cys | Trp | Glu | Ser | Gly | Lys | Val | |
| | | | | | | | | | 85 | | | | | 95 | | |
| ttc | aat | tac | gat | aac | gac | cag | gcc | cag | tta | gaa | gcg | cag | ata | cag | cag | 336 |
| Phe | Asn | Tyr | Asp | Asn | Asp | Gln | Ala | Gln | Leu | Glu | Ala | Gln | Ile | Gln | Gln | |
| | | | | | | | | | 100 | | | | 110 | | | |
| ttt | aat | ccg | cgc | gat | gtt | gcf | ggt | tat | cga | gcf | ttc | ctt | gac | tat | tcg | 384 |
| Phe | Asn | Pro | Arg | Asp | Val | Ala | Gly | Tyr | Arg | Ala | Phe | Leu | Asp | Tyr | Ser | |
| | | | | | | | | | 115 | | | 125 | | | | |
| cgt | gcc | gta | ttc | aat | gag | gcf | tat | ctg | aag | ctc | ggc | act | gtg | cct | ttt | 432 |
| Arg | Ala | Val | Phe | Asn | Glu | Gly | Tyr | Leu | Lys | Leu | Gly | Thr | Val | Pro | Phe | |
| | | | | | | | | | 130 | | | 140 | | | | |
| tta | tcg | tcc | aaa | gac | atg | ctt | cgf | gcc | gcf | ccc | cag | ttg | gca | aag | ctg | 480 |
| Leu | Ser | Phe | Lys | Asp | Met | Leu | Arg | Ala | Ala | Pro | Gln | Leu | Ala | Lys | Leu | |
| | | | | | | | | | 145 | | | 155 | | | 160 | |
| cag | gca | tgg | cgc | agc | gtt | tac | agt | aaa | gtt | gcc | ggc | tac | att | gag | gat | 528 |
| Gln | Ala | Trp | Arg | Ser | Val | Tyr | Ser | Lys | Val | Ala | Gly | Tyr | Ile | Glu | Asp | |
| | | | | | | | | | 165 | | | 170 | | | 175 | |
| gag | cat | ctt | cgf | cag | gcf | ttt | tct | ttt | cac | tcg | ctc | tta | gtg | ggg | ggg | 576 |
| Glu | His | Leu | Arg | Gln | Ala | Phe | Ser | Phe | His | Ser | Leu | Leu | Val | Gly | Gly | |
| | | | | | | | | | 180 | | | 185 | | | 190 | |
| aat | ccg | ttt | gca | acc | tcg | tcc | att | tat | acg | ctg | att | cac | gcf | tta | gaa | 624 |
| Asn | Pro | Phe | Ala | Thr | Ser | Ser | Ile | Tyr | Thr | Leu | Ile | His | Ala | Leu | Glu | |
| | | | | | | | | | 195 | | | 200 | | | 205 | |
| ccg | gaa | tgg | ggc | gtc | tgg | ttt | cca | cgc | ggt | gga | acc | ggt | gcf | ctg | gtc | 672 |
| Arg | Glu | Trp | Gly | Val | Trp | Phe | Pro | Arg | Gly | Gly | Thr | Gly | Ala | Leu | Val | |
| | | | | | | | | | 210 | | | 215 | | | 220 | |
| aat | ggc | atg | atc | aag | ctg | ttt | cag | gat | ctg | ggc | ggc | gaa | gtc | gtg | ctt | 720 |
| Asn | Gly | Met | Ile | Lys | Leu | Phe | Gln | Asp | Leu | Gly | Gly | Gl | Val | Val | Leu | |
| | | | | | | | | | 225 | | | 230 | | | 240 | |
| aac | gcc | cgg | gtc | agt | cat | atg | gaa | acc | gtt | ggg | gac | aag | att | cag | gcc | 768 |
| Asn | Ala | Arg | Val | Ser | His | Met | Glu | Thr | Val | Gly | Asp | Lys | Ile | Gln | Ala | |
| | | | | | | | | | 245 | | | 250 | | | 255 | |
| gtg | cag | ttg | gaa | gac | ggc | aga | cgf | ttt | gaa | acc | tgc | gcf | gtg | gcf | tcg | 816 |
| Val | Gln | Leu | Glu | Asp | Gly | Arg | Arg | Phe | Glu | Thr | Cys | Ala | Val | Ala | Ser | |
| | | | | | | | | | 260 | | | 265 | | | 270 | |
| aac | gct | gat | gtt | gta | cat | acc | tat | cgf | gat | ctg | ctg | tct | cag | cat | ccc | 864 |
| Asn | Ala | Asp | Val | Val | His | Thr | Tyr | Arg | Asp | Leu | Leu | Ser | Gln | His | Pro | |
| | | | | | | | | | 275 | | | 280 | | | 285 | |
| gca | gcc | gct | aag | cag | gcf | aaa | aaa | ctg | caa | tcc | aag | cgt | atg | agt | aac | 912 |
| Ala | Ala | Ala | Lys | Gln | Ala | Lys | Lys | Leu | Gln | Ser | Lys | Arg | Met | Ser | Asn | |
| | | | | | | | | | 290 | | | 295 | | | 300 | |
| tca | ctg | ttt | gta | ctc | tat | ttt | ggt | ctc | aac | cat | cat | cac | gat | caa | ctc | 960 |
| Ser | Leu | Phe | Val | Leu | Tyr | Phe | Gly | Leu | Asn | His | His | His | Asp | Gln | Leu | |
| | | | | | | | | | 305 | | | 310 | | | 315 | |
| gcc | cat | cat | acc | gtc | tgt | ttt | ggg | cca | cgc | tac | cgt | gaa | ctg | att | cac | 1008 |
| Ala | His | His | Thr | Val | Cys | Phe | Gly | Pro | Arg | Tyr | Arg | Glu | Leu | Ile | His | |
| | | | | | | | | | 325 | | | 330 | | | 335 | |
| gaa | att | ttt | aac | cat | gat | ggt | ctg | gct | gag | gat | ttt | tcg | ctt | tat | tta | 1056 |
| Glu | Ile | Phe | Asn | His | Asp | Gly | Leu | Ala | Glu | Asp | Phe | Ser | Leu | Tyr | Leu | |

| 340 | 345 | 350 | |
|---|-----|-----|------|
| cac gca cct tgt gtc acg gat ccg tca ctg gca ccg gaa ggg tgc ggc His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly 355 360 365 | | | 1104 |
| agc tat tat gtg ctg gcg cct gtt cca cac tta ggc acg gcg aac ctc Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu 370 375 380 | | | 1152 |
| gac tgg gcg gta gaa gga ccc cga ctg cgc gat cgt att ttt gac tac Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr 385 390 395 400 | | | 1200 |
| ctt gag caa cat tac atg cct ggc ttg cga agc cag ttg gtg acg cac Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His 405 410 415 | | | 1248 |
| cgt atg ttt acg ccg ttc gat ttc cgc gac gag ctc aat gcc tgg caa Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln 420 425 430 | | | 1296 |
| ggt tcg gcc ttc tcg gtt gaa cct att ctg acc cag agc gcc tgg ttc Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe 435 440 445 | | | 1344 |
| cga cca cat aac cgc gat aag cac att gat aat ctt tat ctg gtt ggc Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly 450 455 460 | | | 1392 |
| gca ggc acc cat cct ggc gcg ggc att ccc ggc gta atc ggc tcg gcg Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala 465 470 475 480 | | | 1440 |
| aag gcg acg gca ggc tta atg ctg gag gac ctg att tga Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile 485 490 | | | 1479 |

<210> 8
 <211> 492
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 <213> *Pantoea stewartii*
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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
 1 5 10 15

Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
 35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
 65 70 75 80

Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90

Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
100 105 110

Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
115 120 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
130 135 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
210 215 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
245 250 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
275 280 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305 310 315 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
325 330 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
340 345 350

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380
 Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
 385 390 395 400
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
 420 425 430
 Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
 450 455 460
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 465 470 475 480
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

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 <213> Pantoea stewartii

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 Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
 1 5 10 15
 gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac 96
 Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
 20 25 30
 tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag 144
 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
 35 40 45
 ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa 192
 Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
 50 55 60
 acg cgt cag gcc tac gcc ggt tcg caa atg cac gag ccc gct ttt gcc 240
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
 65 70 75 80
 gcg ttt cag gag gtc gcg atg gcg cat gat atc gct ccc gcc tac gcg 288
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
 85 90 95
 ttc gac cat ctg gaa ggt ttt gcc atg gat gtg cgc gaa acg cgc tac 336
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| ctg aca ctg gac gat acg ctg cgt tat tgc tat cac gtc gcc ggt gtt Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val 115 120 125 | | | 384 |
| gtg ggc ctg atg atg gcg caa att atg ggc gtt cgc gat aac gcc acg Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr 130 135 140 | | | 432 |
| ctc gat cgc gcc tgc gat ctc ggg ctg gct ttc cag ttg acc aac att Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile 145 150 155 160 | | | 480 |
| gcg cgt gat att gtc gac gat gct cag gtc ggc cgc tgt tat ctg cct Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro 165 170 175 | | | 528 |
| gaa agc tgg ctg gaa gag gaa gga ctg acg aaa gcg aat tat gct gcg Glu Ser Trp Leu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala 180 185 190 | | | 576 |
| cca gaa aac cgg cag gcc tta agc cgt atc gcc ggg cga ctg gta cgg Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg 195 200 205 | | | 624 |
| gaa gcg gaa ccc tat tac gta tca tca atg gcc ggt ctg gca caa tta Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu 210 215 220 | | | 672 |
| ccc tta cgc tcg gcc tgg gcc atc gcg aca gcg aag cag gtg tac cgt Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg 225 230 235 240 | | | 720 |
| aaa att ggc gtc aaa gtt gaa cag gcc ggt aag cag gcc tgg gat cat Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His 245 250 255 | | | 768 |
| cgc cag tcc acg tcc acc gcc gaa aaa tta acg ctt ttg ctg acg gca Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Thr Ala 260 265 270 | | | 816 |
| tcc ggt cag gca gtt act tcc cgg atg aag acg tat cca ccc cgt cct Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro 275 280 285 | | | 864 |
| gct cat ctc tgg cag cgc ccg atc tag Ala His Leu Trp Gln Arg Pro Ile 290 295 | | | 891 |

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 <211> 296
 <212> PRT
 <213> Pantoea stewartii

<400> 10

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1 5 10 15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
35 40 45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
50 55 60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
100 105 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
165 170 175

Glu Ser Trp Leu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
195 200 205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
245 250 255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
260 265 270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
275 280 285

Ala His Leu Trp Gln Arg Pro Ile
290 295

<210> 11
<211> 528
<212> DNA
<213> *Pantoea stewartii*

<220>
<221> CDS
<222> (1)..(528)

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Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1 5 10 15

atg gaa gtc gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg 96
Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30

ggc tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt 144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

gaa gtt aac gat ctc tat gcc gtc gta ttc gcc att gtg tcg att gcc 192
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
50 55 60

ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt 240
Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga 288
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac 336
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga 384
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

aaa gag ggc tgc gtc tcc ttt ggt ttt ctg tac gcg cca ccg tta tct 432
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
130 135 140

aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct 480
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145 150 155 160

gcc aga gat gag cag gac ggg gtc gat acg tct tca tcc ggg aag taa 528
Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
165 170 175

<210> 12
<211> 175
<212> PRT
<213> Pantoea stewartii

<400> 12

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1 5 10 15

Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
 50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
 145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
 165 170 175

<210> 13
 <211> 1860
 <212> DNA
 <213> Methylomonas 16a

<220>
 <221> CDS
 <222> (1)...(1860)

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 Met Ala Leu Ser Lys Asp Phe Pro Leu Leu Asn Ser Ile His Thr Pro
 1 5 10 15

gcg gac ata cgc gcg ctg tcc aag gac cag ctc cag caa ctg gct gac 96
 Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
 20 25 30

gag gtg cgc ggc tat ctg acc cac acg gtc agc att tcc ggc ggc cat 144
 Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
 35 40 45

ttt gcg gcc ggc ctc ggc acc gtg gaa ctg acc gtg gcc ttg cat tat 192
 Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
 50 55 60

gtg ttc aat acc ccc gtc gat cag ttg gtc tgg gac gtg ggc cat cag 240
 Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
 65 70 75 80

gcc tat ccg cac aag att ctg acc ggt cgc aag gag cgc atg ccg acc 288
 Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
 85 90 95

| | |
|---|------|
| att cgc acc ctg ggc ggg gtg tca gcc ttt ccg gcg cgg gac gag agc Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser 100 105 110 | 336 |
| gaa tac gat gcc ttc ggc gtc ggc cat tcc agc acc tcg atc agc gcg Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala 115 120 125 | 384 |
| gca ctg ggc atg gcc att gcg tcg cag ctg cgc ggc gaa gac aag aag Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys 130 135 140 | 432 |
| atg gta gcc atc atc ggc gac ggt tcc atc acc ggc ggc atg gcc tat Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr 145 150 155 | 480 |
| gag gcg atg aat cat gcc ggc gat gtg aat gcc aac ctg ctg gtg atc Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile 165 170 175 | 528 |
| ttg aac gac aac gat atg tcg atc tcg ccg ccg gtc ggg gcg atg aac Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn 180 185 190 | 576 |
| aat tat ctg acc aag gtg ttg tcg agc aag ttt tat tcg tcg gtg cg Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg 195 200 205 | 624 |
| gaa gag agc aag aaa gct ctg gcc aag atg ccg tcg gtg tgg gaa ctg Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu 210 215 220 | 672 |
| gcg cgc aag acc gag gaa cac gtg aag ggc atg atc gtg ccc ggt acc Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr 225 230 235 240 | 720 |
| ttg ttc gag gaa ttg ggc ttc aat tat ttc ggc ccg atc gac ggc cat Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His 245 250 255 | 768 |
| gat gtc gag atg ctg gtg tcg acc ctg gaa aat ctg aag gat ttg acc Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr 260 265 270 | 816 |
| ggg ccg gta ttc ctg cat gtg gtg acc aag aag ggc aaa ggc tat gcg Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala 275 280 285 | 864 |
| cca gcc gag aaa gac ccg ttg gcc tac cat ggc gtg acc gct ttc gat Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp 290 295 300 | 912 |
| ccg acc aag gat ttc ctg ccc aag gcg gcg ccg tcg ccg cat ccg acc Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr 305 310 315 320 | 960 |
| tat acc gag gtg ttc ggc cgc tgg ctg tgc gac atg gcg gct caa gac Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp 325 330 335 | 1008 |
| gag cgc ttg ctg ggc atc acg ccg gcg atg cgc gaa ggc tct ggt ttg Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu 340 345 350 | 1056 |
| gtg gaa ttc tca cag aaa ttt ccg aat cgc tat ttc gat gtc gcc atc Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile 355 360 365 | 1104 |
| gcc gag cag cat gcg gtg acc ttg gcc ggc cag gcc tgc cag ggc Page 18 | 1152 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Ala | Glu | Gln | His | Ala | Val | Thr | Leu | Ala | Ala | Gly | Gln | Ala | Cys | Gln | Gly | |
| 370 | | | | 375 | | | | | | 380 | | | | | | |
| gcc | aag | ccg | gtg | gtg | gcf | att | tat | tcc | acc | ttc | ctg | caa | cgc | ggt | tac | 1200 |
| Ala | Lys | Pro | Val | Val | Ala | Ile | Tyr | Ser | Thr | Phe | Leu | Gln | Arg | Gly | Tyr | |
| 385 | | | | 390 | | | | | 395 | | | | | | 400 | |
| gat | cag | ttg | atc | cac | gac | gtg | gcc | ttg | cag | aac | tta | gat | atg | ctc | ttt | 1248 |
| Asp | Gln | Leu | Ile | His | Asp | Val | Ala | Leu | Gln | Asn | Leu | Asp | Met | Leu | Phe | |
| | | | | 405 | | | | 410 | | | | | | 415 | | |
| gca | ctg | gat | cgt | gcc | ggc | ttg | gtc | ggc | ccg | gat | gga | ccg | acc | cat | gct | 1296 |
| Ala | Leu | Asp | Arg | Ala | Gly | Leu | Val | Gly | Pro | Asp | Gly | Pro | Thr | His | Ala | |
| | | | | 420 | | | | 425 | | | | 430 | | | | |
| ggc | gcc | ttt | gat | tac | agc | tac | atg | cgc | tgt | att | ccg | aac | atg | ctg | atc | 1344 |
| Gly | Ala | Phe | Asp | Tyr | Ser | Tyr | Met | Arg | Cys | Ile | Pro | Asn | Met | Leu | Ile | |
| | | | | 435 | | | 440 | | 445 | | | | | | | |
| atg | gct | cca | gcc | gac | gag | aac | gag | tgc | agg | cag | atg | ctg | acc | acc | ggc | 1392 |
| Met | Ala | Pro | Ala | Asp | Glu | Asn | Glu | Cys | Arg | Gln | Met | Leu | Thr | Thr | Gly | |
| | | | | 450 | | | 455 | | 460 | | | | | | | |
| ttc | caa | cac | cat | ggc | ccg | gct | tcg | gtg | cgc | tat | ccg | cgc | ggc | aaa | ggg | 1440 |
| Phe | Gln | His | His | Gly | Pro | Ala | Ser | Val | Arg | Tyr | Pro | Arg | Gly | Lys | Gly | |
| | | | | 465 | | | 470 | | 475 | | | | | 480 | | |
| ccc | ggg | gcf | gca | atc | gat | ccg | acc | ctg | acc | gcf | ctg | gag | atc | ggc | aag | 1488 |
| Pro | Gly | Ala | Ala | Ile | Asp | Pro | Thr | Leu | Thr | Ala | Leu | Glu | Ile | Gly | Lys | |
| | | | | 485 | | | 490 | | | | | | | 495 | | |
| gcc | gaa | gtc | aga | cac | cac | ggc | agc | cgc | atc | gcc | att | ctg | gcc | tgg | ggc | 1536 |
| Ala | Glu | Val | Arg | His | His | Gly | Ser | Arg | Ile | Ala | Ile | Leu | Ala | Trp | Gly | |
| | | | | 500 | | | 505 | | | | | | | 510 | | |
| agc | atg | gtc | acg | cct | gcc | gtc | gaa | gcc | ggc | aag | cag | ctg | ggc | gcf | acg | 1584 |
| Ser | Met | Val | Thr | Pro | Ala | Val | Glu | Ala | Gly | Lys | Gln | Leu | Gly | Ala | Thr | |
| | | | | 515 | | | 520 | | | | 525 | | | | | |
| gtg | gtg | aac | atg | cgt | ttc | gtc | aag | ccg | ttc | gat | caa | gcc | ttg | gtg | ctg | 1632 |
| Val | Val | Asn | Met | Arg | Phe | Val | Lys | Pro | Phe | Asp | Gln | Ala | Leu | Val | Leu | |
| | | | | 530 | | | 535 | | | | 540 | | | | | |
| gaa | ttg | gcc | agg | acg | cac | gat | gtg | ttc | gtc | acc | gtc | gag | gaa | aac | gtc | 1680 |
| Glu | Leu | Ala | Arg | Thr | His | Asp | Val | Phe | Val | Thr | Val | Glu | Glu | Asn | Val | |
| | | | | 545 | | | 550 | | | | 555 | | | | 560 | |
| atc | gcc | ggc | ggc | gct | ggc | agt | gcf | atc | aac | acc | ttc | ctg | cag | gcf | cag | 1728 |
| Ile | Ala | Gly | Gly | Ala | Gly | Ser | Ala | Ile | Asn | Thr | Phe | Leu | Gln | Ala | Gln | |
| | | | | 565 | | | 570 | | | | | | | 575 | | |
| aag | gtg | ctg | atg | ccg | gtc | tgc | aac | atc | ggc | ctg | ccc | gac | ccg | ttc | gtc | 1776 |
| Lys | Val | Leu | Met | Pro | Val | Cys | Asn | Ile | Gly | Leu | Pro | Asp | Arg | Phe | Val | |
| | | | | 580 | | | 585 | | | | | | | 590 | | |
| gag | caa | ggt | agt | cgc | gag | gaa | ttg | ctc | agc | ctg | gtc | ggc | ctc | gac | agc | 1824 |
| Glu | Gln | Gly | Ser | Arg | Glu | Gl | Leu | Leu | Ser | Leu | Val | Gly | Leu | Asp | Ser | |
| | | | | 595 | | | 600 | | | | | | | 605 | | |
| aag | ggc | atc | tcc | gcc | acc | atc | gaa | cag | ttt | tgc | gtc | | | | | 1860 |
| Lys | Gly | Ile | Phe | Ala | Thr | Ile | Glu | Gln | Phe | Cys | Ala | | | | | |
| | | | | 610 | | | 615 | | | | 620 | | | | | |

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 <213> Methylomonas 16a

<400> 14

Met Ala Leu Ser Lys Asp Phe Pro Leu Leu Asn Ser Ile His Thr Pro
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Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
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Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
35 40 45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
50 55 60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65 70 75 80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
85 90 95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
100 105 110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
115 120 125

Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
130 135 140

Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145 150 155 160

Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
165 170 175

Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
180 185 190

Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
195 200 205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
210 215 220

Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
225 230 235 240

Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
245 250 255

Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
260 265 270

Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
275 280 285

Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
290 295 300

Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
305 310 315 320

Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
325 330 335

Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
340 345 350

Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
355 360 365

Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
370 375 380

Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
385 390 395 400

Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
405 410 415

Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
420 425 430

Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
435 440 445

Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
450 455 460

Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
465 470 475 480

Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
485 490 495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
500 505 510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
515 520 525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
530 535 540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545 550 555 560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
565 570 575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
580 585 590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
595 600 605

Lys Gly Ile Phe Ala Thr Ile Glu Gln Phe Cys Ala
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<213> Methylomonas 16a

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1 5 10

ttc tgt gcc ggc gtg gac cgg gcc att gaa att gtc gat caa gcc atc 99
Phe Cys Ala Gly Val Asp Arg Ala Ile Glu Ile Val Asp Gln Ala Ile
15 20 25

gaa gcc ttt ggt gcg ccg att tat gtg cgg cac gag gtg gtg cat aac 147
Glu Ala Phe Gly Ala Pro Ile Tyr Val Arg His Glu Val Val His Asn
30 35 40

cgc acc gtg gtc gat gga ctg aaa caa aaa ggt gcg gtg ttc atc gag 195
Arg Thr Val Val Asp Gly Leu Lys Gln Lys Gly Ala Val Phe Ile Glu
45 50 55

gaa cta agc gat gtg ccg gtg ggt tcc tac ttg att ttc agc gcg cac 243
Glu Leu Ser Asp Val Pro Val Gly Ser Tyr Leu Ile Phe Ser Ala His
60 65 70

ggc gta tcc aag gag gtg caa cag gaa gcc gag gag cgc cag ttg acg 291
Gly Val Ser Lys Glu Val Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr
75 80 85 90

gta ttc gat gcg act tgt ccg ctg gtg acc aaa gtg cac atg cag gtt 339
Val Phe Asp Ala Thr Cys Pro Leu Val Thr Lys Val His Met Gln Val
95 100 105

gcc aag cat gcc aaa cag ggc cga gaa gtg att ttg atc ggc cac gcc 387
Ala Lys His Ala Lys Gln Gly Arg Glu Val Ile Leu Ile Gly His Ala
110 115 120

ggt cat ccg gaa gtg gaa ggc acg atg ggc cag tat gaa aaa tgc acc 435
Gly His Pro Glu Val Glu Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr
125 130 135

gaa ggc ggc att tat ctg gtc gaa act ccg gaa gac gta cgc aat 483
Glu Gly Gly Ile Tyr Leu Val Glu Thr Pro Glu Asp Val Arg Asn

| | | | |
|---|-----|-----|-----|
| 140 | 145 | 150 | |
| ttg aaa gtc aac aat ccc aat gat ctg gcc tat gtg acg cag acg acc | | | |
| Leu Lys Val Asn Asn Pro Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr | | | |
| 155 | 160 | 165 | 170 |
| ttg tcg atg acc gac acc aag gtc atg gtg gat ggc tta cgc gaa caa | | | |
| Leu Ser Met Thr Asp Thr Lys Val Met Val Asp Ala Leu Arg Glu Gln | | | |
| 175 | 180 | | 185 |
| ttt ccg tcc att aag gag caa aaa aag gac gat att tgt tac gcg acg | | | |
| Phe Pro Ser Ile Lys Glu Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr | | | |
| 190 | 195 | 200 | |
| caa aac cgt cag gat gcg gtg cat gat ctg gcc aag att tcc gac ctg | | | |
| Gln Asn Arg Gln Asp Ala Val His Asp Leu Ala Lys Ile Ser Asp Leu | | | |
| 205 | 210 | 215 | |
| att ctg gtt gtc ggc tct ccc aat agt tcg aat tcc aac cgt ttg cgt | | | |
| Ile Leu Val Val Gly Ser Pro Asn Ser Asn Ser Asn Arg Leu Arg | | | |
| 220 | 225 | 230 | |
| gaa atc gcc gtg caa ctc ggt aaa ccc gct tat ttg atc gat act tac | | | |
| Glu Ile Ala Val Gln Leu Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr | | | |
| 235 | 240 | 245 | 250 |
| cag gat ttg aag caa gat tgg ctg gag gga att gaa gta gtc ggg gtt | | | |
| Gln Asp Leu Lys Gln Asp Trp Leu Glu Gly Ile Glu Val Val Gly Val | | | |
| 255 | 260 | 265 | |
| acc gcg ggc gct tcg gcg ccg gaa gtg ttg gtg cag gaa gtg atc gat | | | |
| Thr Ala Gly Ala Ser Ala Pro Glu Val Leu Val Gln Glu Val Ile Asp | | | |
| 270 | 275 | 280 | |
| caa ctg aag gca tgg ggc ggc gaa acc act tcg gtc aga gaa aac agc | | | |
| Gln Leu Lys Ala Trp Gly Gly Glu Thr Thr Ser Val Arg Glu Asn Ser | | | |
| 285 | 290 | 295 | |
| ggc atc gag gaa aag gta gtc ttt tcg att ccc aag gag ttg aaa aaa | | | |
| Gly Ile Glu Glu Lys Val Val Phe Ser Ile Pro Lys Glu Leu Lys Lys | | | |
| 300 | 305 | 310 | |
| cat atg caa gcg tgatcaa | | | |
| His Met Gln Ala | | | |
| 315 | | | |

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 <213> Methylomonas 16a

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Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro
 20 25 30

Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly
 35 40 45

Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro
 50 55 60

Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val
65 70 75 80

Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
85 90 95

Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
100 105 110

Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
115 120 125

Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Ile Tyr
130 135 140

Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro
145 150 155 160

Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr
165 170 175

Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu
180 185 190

Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala
195 200 205

Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser
210 215 220

Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu
225 230 235 240

Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp
245 250 255

Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala
260 265 270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly
275 280 285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val
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Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala
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<213> Methylomonas 16a

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| gagcgatattc ga atg aaa ggt att tgc ata ttg ggc gct acc ggt tcg atc | 111 |
| Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile | |
| 1 5 10 | |
| ggt gtc agc acg ctg gat gtc gtt gcc agg cat ccg gat aaa tat caa | 159 |
| Gly Val Ser Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln | |
| 15 20 25 | |
| gtc gtt gcg ctg acc gcc aac ggc aat atc gac gca ttg tat gaa caa | 207 |
| Val Val Ala Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln | |
| 30 35 40 45 | |
| tgc ctg gcc cac cat ccg gag tat gcg gtc gtc atg gaa agc aag | 255 |
| Cys Leu Ala His His Pro Glu Tyr Ala Val Val Met Glu Ser Lys | |
| 50 55 60 | |
| gta gca gag ttc aaa cag cgc att gcc gct tcg ccg gta gcg gat atc | 303 |
| Val Ala Glu Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile | |
| 65 70 75 | |
| aag gtc ttg tcg ggt agc gag gcc ttg caa cag gtc gcc acg ctg gaa | 351 |
| Lys Val Leu Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu | |
| 80 85 90 | |
| aac gtc gat acg gtc atg gcg gct atc gtc ggc gcg gcc gga ttg ttg | 399 |
| Asn Val Asp Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu | |
| 95 100 105 | |
| ccg acc ttg gcc gcg gcc aag gcc ggc aaa acc gtc ctg ttg gcc aac | 447 |
| Pro Thr Leu Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn | |
| 110 115 120 125 | |
| aag gaa gcc ttg gtc atg tcg gga caa atc ttc atg cag gcc gtc agc | 495 |
| Lys Glu Ala Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser | |
| 130 135 140 | |
| gat tcc ggc gct gtc ttg ctg ccg ata gac agc gag cac aac gcc atc | 543 |
| Asp Ser Gly Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile | |
| 145 150 155 | |
| ttt cag tgc atg ccg gcg ggt tat acg cca ggc cat aca gcc aaa cag | 591 |
| Phe Gln Cys Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln | |
| 160 165 170 175 | |
| gcg cgc cgc att tta ttg acc gct tcc ggt ggc cca ttt cga cggt acg | 639 |
| Ala Arg Arg Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr | |
| 175 180 185 | |
| ccg ata gaa acg ttg tcc agc gtc acg ccg gat cag gcc gtt gcc cat | 687 |
| Pro Ile Glu Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His | |
| 190 195 200 205 | |
| cct aaa tgg gac atg ggg cgc aag att tcg gtc gat tcc gcc acc atg | 735 |
| Pro Lys Trp Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met | |
| 210 215 220 | |
| atg aac aaa ggt ctc gaa ctg atc gaa gcc tgc ttg ttg ttc aac atg | 783 |
| Met Asn Lys Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met | |
| 225 230 235 | |

| | |
|---|------|
| gag ccc gac cag att gaa gtc gtc att cat ccg cag agc atc att cat | 831 |
| Glu Pro Asp Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His | |
| 240 245 250 | |
| tcg atg gtg gac tat gtc gat ggt tcg gtt ttg gcg cag atg ggt aat | 879 |
| Ser Met Val Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn | |
| 255 260 265 | |
| ccc gac atg cgc acg ccg ata gcg cac gcg atg gcc tgg ccg gaa cgc | 927 |
| Pro Asp Met Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg | |
| 270 275 280 285 | |
| ttt gac tct ggt gtg gcg ccg ctg gat att ttc gaa gta ggg cac atg | 975 |
| Phe Asp Ser Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met | |
| 290 295 300 | |
| gat ttc gaa aaa ccc gac ttg aaa cggttt cct tgt ctg aga ttg gct | 1023 |
| Asp Phe Glu Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala | |
| 305 310 315 | |
| tat gaa gcc atc aag tct ggt gga att atg cca acg gta ttg aac gca | 1071 |
| Tyr Glu Ala Ile Lys Ser Gly Ile Met Pro Thr Val Leu Asn Ala | |
| 320 325 330 | |
| gcc aat gaa att gct gtc gaa gcgttt tta aat gaa gaa gtc aaa ttc | 1119 |
| Ala Asn Glu Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe | |
| 335 340 345 | |
| act gac atc gcg gtc atc atc gag cgc agc atg gcc cag ttt aaa ccg | 1167 |
| Thr Asp Ile Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro | |
| 350 355 360 365 | |
| gac gat gcc ggc agc ctc gaa ttgttt cag gcc gat caa gat gcg | 1215 |
| Asp Asp Ala Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala | |
| 370 375 380 | |
| cgc gag gtg gct aga gac atc atc aag acc ttg gta gct | 1254 |
| Arg Glu Val Ala Arg Asp Ile Ile Lys Thr Leu Val Ala | |
| 385 390 | |

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 <212> PRT
 <213> Methylomonas 16a

<400> 18

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 20 25 30

Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
 35 40 45

His His Pro Glu Tyr Ala Val Val Met Glu Ser Lys Val Ala Glu
 50 55 60

Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
 65 70 75 80

Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
 Page 26

85

90

95

Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
 100 105 110

Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
 115 120 125

Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
 130 135 140

Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
 145 150 155 160

Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
 165 170 175

Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
 180 185 190

Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
 195 200 205

Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
 210 215 220

Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
 225 230 235 240

Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
 245 250 255

Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
 260 265 270

Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
 275 280 285

Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
 290 295 300

Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala
 305 310 315 320

Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu
 325 330 335

Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile
 340 345 350

Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
 355 360 365

Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala Arg Glu Val
370 375 380

Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
385 390

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25

<210> 20
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Primer #2 for amplification of crt gene cluster

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gagaaattat gttgtggatt tggaaatgc

28

<210> 21
<211> 61
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(dxs)

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60

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61

<210> 22
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<212> DNA
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<220>
<223> Primer 5'kan(idi)

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60

tgtag

65

<210> 23
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(ygbBP)

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|--|----|--|
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| gacgcgtcga agcgcgacaca gtctgcgggg caaaacaatc gataacgtct tgagcgattg | 60 | |
| tgttag | 65 | |
| | | |
| <210> 24 | | |
| <211> 60 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| | | |
| <220> | | |
| <223> Primer 5'kan(ispAdxs) | | |
| | | |
| <400> 24 | | |
| accatgacgg ggcgaaaaat attgagagtc agacattcat gtgtaggctg gagctgcttc | 60 | |
| | | |
| <210> 25 | | |
| <211> 64 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| | | |
| <220> | | |
| <223> Primer 3'kan | | |
| | | |
| <400> 25 | | |
| gaagacgaaa gggcctcgtg atacgcctat ttttataagggt tataatgaata tcctccttag | 60 | |
| ttcc | 64 | |
| | | |
| <210> 26 | | |
| <211> 50 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
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| <220> | | |
| <223> Primer 5'-T5 | | |
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| <400> 26 | | |
| ctaaggagga tattcatata acctataaaa ataggcgtat cacgaggccc | 50 | |
| | | |
| <210> 27 | | |
| <211> 70 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| | | |
| <220> | | |
| <223> Primer 3'-T5(dx5) | | |
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| <400> 27 | | |
| ggagtcgacc agtgcgcaggg tcgggtatgg ggcaatatca aaactcatag ttaattctc | 60 | |
| ctctttaatg | 70 | |
| | | |
| <210> 28 | | |
| <211> 68 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| | | |
| <220> | | |
| <223> Primer 3'-T5(idi) | | |
| | | |
| <400> 28 | | |
| tgggaactcc ctgtgcattc aataaaatga cgtgtccgt ttgcataatg aatttctcct | 60 | |

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| ctttaatg | 68 |
| <210> 29 | |
| <211> 68 | |
| <212> DNA | |
| <213> Artificial sequence | |
| <220> | |
| <223> Primer 3'-T5(ygbBP) | |
| <400> 29 | |
| cggccgcccgg aaccacggcg caaacatcca aatgagtggc tgccatagtt aatttctcct | 60 |
| ctttaatg | 68 |
| <210> 30 | |
| <211> 62 | |
| <212> DNA | |
| <213> Artificial sequence | |
| <220> | |
| <223> Primer 3'-T5(ispAdxs) | |
| <400> 30 | |
| cctgcttaac gcaggcttcg agttgctgcg gaaagtccat agttaatttc tccttttaa | 60 |
| tg | 62 |
| <210> 31 | |
| <211> 65 | |
| <212> DNA | |
| <213> Artificial sequence | |
| <220> | |
| <223> Primer 5'-kanT5(ispB) | |
| <400> 31 | |
| accataaaacc ctaagttgcc tttgttcaca gtaaggtaat cggggcgtct tgagcgattg | 60 |
| tgttag | 65 |
| <210> 32 | |
| <211> 67 | |
| <212> DNA | |
| <213> Artificial sequence | |
| <220> | |
| <223> Primer 3'-kanT5(ispB) | |
| <400> 32 | |
| cgcctatatct tgcgcggtta actcattgat ttttctaaa ttcatagtttta atttctcctc | 60 |
| tttaatg | 67 |
| <210> 33 | |
| <211> 156 | |
| <212> DNA | |
| <213> Artificial sequence | |
| <220> | |
| <223> Phage T5 promoter sequence | |
| <400> 33 | |

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| ctataaaaat aggcttatca cgaggccctt tcgtttcac ctcgagaaat cataaaaaat | 60 |
| ttatttgcctt tgtgagcgga taacaattat aatagattca atttgagcg gataacaatt | 120 |
| tcacacagaa ttcattaaag aggagaaatt aactca | 156 |
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| <210> 34 | |
| <211> 65 | |
| <212> DNA | |
| <213> Artificial sequence | |
| | |
| <220> | |
| <223> Primer 5'-kanT5(dxr16a) | |
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| <400> 34 | |
| cactaacgccc cgcacattgc tgcgggcttt ttgattcatt tcgcacgtct tgagcgattg | 60 |
| tgttag | 65 |
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| <210> 35 | |
| <211> 65 | |
| <212> DNA | |
| <213> Artificial sequence | |
| | |
| <220> | |
| <223> Primer 5'-kanT5(dxr16a) | |
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| <400> 35 | |
| taaaggggcta agagtagtgt gctcttagcc cttaattacg tttcccgctct tgagcgattg | 60 |
| tgttag | 65 |
| | |
| <210> 36 | |
| <211> 65 | |
| <212> DNA | |
| <213> Artificial sequence | |
| | |
| <220> | |
| <223> Primer 5'-kanT5(lytB16a) | |
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| <400> 36 | |
| ctacaactgg cgagatgcat agcgagtata atttgtatgg tgcgtcgat tgagcgattg | 60 |
| tgttag | 65 |
| | |
| <210> 37 | |
| <211> 51 | |
| <212> DNA | |
| <213> Artificial sequence | |
| | |
| <220> | |
| <223> Primer 3'-kanT5(dxr16a) | |
| | |
| <400> 37 | |
| agtagaggga agtctttgga aagagccata gttttttct ctttttaat g | 51 |
| | |
| <210> 38 | |
| <211> 51 | |
| <212> DNA | |
| <213> Artificial sequence | |
| | |
| <220> | |
| <223> Primer 3'-kanT5(dxr16a) | |

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|--------------------------------|------------|-------------|------------|------------|------------|----|
| <400> 38 | | | | | | |
| acggtgccgc | cgcaatgatg | ctgtccacca | gttaatttct | cctctttaat | g | 51 |
| <210> 39 | | | | | | |
| <211> 51 | | | | | | |
| <212> DNA | | | | | | |
| <213> Artificial sequence | | | | | | |
| <220> | | | | | | |
| <223> Primer 3'-kanT5(lytB16a) | | | | | | |
| <400> 39 | | | | | | |
| ccacgggggt | ttgcgagtag | gatttgacata | gttaatttct | cctctttaat | g | 51 |
| <210> 40 | | | | | | |
| <211> 55 | | | | | | |
| <212> DNA | | | | | | |
| <213> Artificial sequence | | | | | | |
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| <223> Primer 5'-(dxs16a) | | | | | | |
| <400> 40 | | | | | | |
| acagaattca | ttaaagagga | gaaattaact | atggctctt | ccaaagactt | ccctc | 55 |
| <210> 41 | | | | | | |
| <211> 55 | | | | | | |
| <212> DNA | | | | | | |
| <213> Artificial sequence | | | | | | |
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| <223> Primer 5'-(dxr16a) | | | | | | |
| <400> 41 | | | | | | |
| acagaattca | ttaaagagga | gaaattaact | ggtggacagc | atcattgcgg | cgcca | 55 |
| <210> 42 | | | | | | |
| <211> 55 | | | | | | |
| <212> DNA | | | | | | |
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| <223> Primer 5'-(lytB16a) | | | | | | |
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| acagaattca | ttaaagagga | gaaattaact | atgcaaatcg | tactcgcaa | cccc | 55 |
| <210> 43 | | | | | | |
| <211> 68 | | | | | | |
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| <223> Primer 3'-(dxs16a) | | | | | | |
| <400> 43 | | | | | | |
| aggagcgaag | tgattatcg | tatgctgttc | atatagcctc | gaattatcaa | gcgcaaaact | 60 |
| gttcgatg | | | | | | 68 |
| <210> 44 | | | | | | |
| <211> 67 | | | | | | |
| <212> DNA | | | | | | |

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| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer 3'-(dxr16a) | | |
| <400> 44 | | |
| ggcattttca ctctggcaat gcgcataaac gctttcaaag tcctgttaag ctaccaaggt | 60 | |
| cttgatg | 67 | |
| <210> 45 | | |
| <211> 68 | | |
| <212> DNA | | |
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| <220> | | |
| <223> Primer 3'-(lytB16a) | | |
| <400> 45 | | |
| agtggcggac gggcaaacaa ggtaacata ggatcaatga gggttattga tcacgcttgc | 60 | |
| atatgttt | 68 | |
| <210> 46 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer T-kan | | |
| <400> 46 | | |
| accggatatac accacttatac tgctc | 25 | |
| <210> 47 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-ispa | | |
| <400> 47 | | |
| cctaataatg cgccatactg catgg | 25 | |
| <210> 48 | | |
| <211> 32 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer T-T5 | | |
| <400> 48 | | |
| taacctataa aataggcgat atcacgaggc cc | 32 | |
| <210> 49 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-idi | | |

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| <400> 49 | | |
| tcatgctgac ctggtaagg aatcc | | 25 |
| <210> 50 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-dxs(16a) | | |
| <400> 50 | | |
| gcgatattgt atgtctgatt cagga | | 25 |
| <210> 51 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-lytB(16a) | | |
| <400> 51 | | |
| tccactggat gcggaaagct ggcag | | 25 |
| <210> 52 | | |
| <211> 26 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-dxs | | |
| <400> 52 | | |
| tggcaacagt cgtagctcct gggtgg | | 26 |
| <210> 53 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-ygb | | |
| <400> 53 | | |
| ccagcagcgc atgcaccgag tgttc | | 25 |
| <210> 54 | | |
| <211> 21 | | |
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| <220> | | |
| <223> Primer Tn5PCRF | | |
| <400> 54 | | |
| gctgagttga aggatcagat c | | 21 |
| <210> 55 | | |
| <211> 21 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |

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| <223> Primer Tn5PCRR | | |
| <400> 55 | | 21 |
| cgagcaagac gtttcccgtt g | | |
| <210> 56 | | |
| <211> 25 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer Kan-2 FP-1 | | |
| <400> 56 | | 25 |
| acctacaaca aagctctcat caacc | | |
| <210> 57 | | |
| <211> 25 | | |
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| <213> Artificial sequence | | |
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| <400> 57 | | 25 |
| gcaatgtAAC atcagagatt ttgag | | |
| <210> 58 | | |
| <211> 20 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer Y15_F | | |
| <400> 58 | | 20 |
| ggatcgatct tgagatgacc | | |
| <210> 59 | | |
| <211> 24 | | |
| <212> DNA | | |
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| <220> | | |
| <223> Primer Y15_R | | |
| <400> 59 | | 24 |
| gcttcgtaa tttcgcatt tctg | | |
| <210> 60 | | |
| <211> 25 | | |
| <212> DNA | | |
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| <223> Primer T-Tn5yjeR | | |
| <400> 60 | | 25 |
| gcaatgtAAC atcagagatt ttgag | | |
| <210> 61 | | |
| <211> 24 | | |

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| <212> DNA | | |
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| <220> | | |
| <223> Primer B-yjeR | | |
| <400> 61 | | 24 |
| gctttcgtaa ttttcgcatt tctg | | |
| <210> 62 | | |
| <211> 26 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Primer B-ispb | | |
| <400> 62 | | 26 |
| agtacagcaa tcatcgacg aatacg | | |
| <210> 63 | | |
| <211> 1845 | | |
| <212> DNA | | |
| <213> Artificial sequence | | |
| <220> | | |
| <223> Sequence yjeR::Tn5 mutant gene (transposon disrupted yjeR) | | |
| <400> 63 | | |
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| gaaaatagca tgagtgccaa tgaaaacaac ctgatttggc tcgatcttga gatgaccggc | 120 | |
| ctggatcccg agcgcgatcg cattattgag attgccacgc tggtagccga tgccaacctg | 180 | |
| aatattctgg cagaagggcc gaccattgca gtacaccgt ctgtatgaaca gctggcgctg | 240 | |
| atggatgact ggaacgtgcg caccatacc gccagcgggc tggtagagcg cgtgaaagcg | 300 | |
| agcacgatgg gcgatcgaa agctgaactg gcaacgctcg aattttaaa acagtgggtg | 360 | |
| cctgcggaa aatcgccgat ttgcggtaac agcatcggtc aggaccgtcg tttcctgttt | 420 | |
| aaatacatgc cggagctgga agcctacttc cactaccgtt atctcgatgt cagcacccctg | 480 | |
| aaagagctgg cgccgcgtg gaagccggaa attctggatg gttttaccaa gcaggggacg | 540 | |
| catcaggcga tggatgatcc cctgtatcg gtggcggagc tggcttacta cctgtctctt | 600 | |
| atacacatct caaccctgaa gcttgcattgc ctgcaggctcg actcttagagg atccccgcca | 660 | |
| cggttgatga gagcttggatcc tggatggac cagttggatg ttttgaactt ttgcggcc | 720 | |
| acggaaacggt ctgcgttgc gggaaagatgc gtgatctgat ccttcaactc agcaaaagtt | 780 | |
| cgatttattc aacaaagccg ccgtcccgat aagtcaacgt aatgctctgc cagtgatgt | 840 | |
| accaattaac caattctgat tagaaaaact catcgagcat caaatgaaac tgcaatttat | 900 | |
| tcatatcagg attatcaata ccatatcccccc gaaaaagccg tttctgtat gaaggagaaa | 960 | |
| actcaccgag gcagttccat agatggccaa gatcctggta tcggctcg attccgactc | 1020 | |
| gtccaaacatc aataacaacct attaatttcc cctcgtaaa aataaggtt tcaagtgaga | 1080 | |
| aatcaccatg agtgacgact gaatccgggtg agaatggccaa aagtttatgc atttcttcc | 1140 | |

| | |
|--|------|
| agacttgttc aacaggccag ccattacgct cgtcatcaaa atcaactcgca tcaaccaaac | 1200 |
| cgttattcat tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac | 1260 |
| aattacaaac aggaatcgaa tgcaaccggc gcaggaacac tgccagcgc a tcaacaatat | 1320 |
| tttcacctga atcaggatat tcttctaata cctggaatgc tgaaaaatccg gggatcgca | 1380 |
| tggtgagtaa ccatgcatca tcaggagtaa ggataaaaatg cttgatggtc ggaagaggca | 1440 |
| taaattccgt cagccagttt agtctgacca tctcatctgt aacatcattt gcaacgctac | 1500 |
| ctttgccatg tttcagaaac aactctggcg catcgggctt cccatacaat cgatagattt | 1560 |
| tcgcacctga ttgcccaca ttatcgcgag cccattata cccatataaa tcagcatcca | 1620 |
| tgttggatt taatcgccgc ctcgagcaag acgtttcccg ttgaatatgg ctcataacac | 1680 |
| cccttgtatt actgtttatg taagcagaca gttttattgt tcatgatgat atattttat | 1740 |
| cttgcataat gtaacatcg agatttttagt acacaattca tcgatgatgg ttgagatgtg | 1800 |
| tataagagac aggcttacta ccgcgagcat tttatcaagc tgtaa | 1845 |

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<220>
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| gttttccatg agcaaactga aacgaaaaa tca tcgctctggta gtgaataccca cgacgatttc | 120 |
| cgccagtttc tacacatata ttgcgaagat gtggcggtt acggtaaaaaa cctggcctat | 180 |
| ttccctaaag gttttattga gaatatgttt ttcgtctcag ccaatccctg ggtgagttc | 240 |
| accagtttg atttaaacgt ggcataatgt gacaacttct tcgccccgt tttcaccatg | 300 |
| ggcaaatatt atacgcaagg cgacaagggtg ctgatgccgc tggcgattca gtttcatcat | 360 |
| gccgtctgtg atggcttcca tgtcggcaga atgcttaatg aattacaaca gtactgcgt | 420 |
| gagtggcagg gcggggcgta attttttaa ggcagttatt ggtgcctaga aatattttat | 480 |
| ctgattaata agatgatctt cttgagatcg tttggctctg cgcgtaatct cttgctctga | 540 |
| aaacaaaaaa accgccttc agggcggtt ttcaagggtt ctctgagcta ccaactcttt | 600 |
| gaaccgaggt aactggctt gaggagcgc gtcacaaaaa cttgtccctt cagtttagcc | 660 |
| ttaaccggcg catgacttca agactaactc ctctaaatca attaccagt gctgctgcc | 720 |
| gtgggtcttt tgcgtctt tccgggttgg actcaagacg atagttaccg gataaggcgc | 780 |
| agcggtcgga ctgaacgggg ggttcgtgca tacagtccag cttggagcga actgcctacc | 840 |
| cgaaactgag tgtcaggcgt ggaatgagac aaacgcggcc ataacagcgg aatgacaccg | 900 |
| gtaaaccgaa aggcaggaac aggagagcgc acgagggagc cgccagggga aacgccttgtt | 960 |
| atctttatag tcctgtcggg tttcgccacc actgattga gcgtcagatt tcgtatgt | 1020 |
| tgtcaggggg gcggagccta tggaaaaacg gctttgccgc ggccctctca cttccctgtt | 1080 |

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|---|------|
| aagtatcttc ctggcatctt ccaggaaatc tccgccccgt tcgtaagcca tttccgctcg | 1140 |
| ccgcagtcga acgaccgagc gtagcgagtc agtgagcgag gaagcggaat atatcctgta | 1200 |
| tcacatattc tgctgacgca ccgggtgcagc ctttttctc ctgccacatg aagcacttca | 1260 |
| ctgacaccct catcagtgcc aacatagtaa gccagtatac acactccgct agcggccaat | 1320 |
| acgcaaaccg cctctcccccgcg cgcgttggcc gattcattaa tgca gctggc acgacaggtt | 1380 |
| tcccgactgg aaagcggca gtgagcgca cgcaattaat gtgagttgc tcactcatta | 1440 |
| ggcaccccg gctttacact ttatgcttcc ggctcgatg ttgtgtggaa ttgtgagcgg | 1500 |
| ataacaattt cacacagggaa acagctatga ccatgattac gaattcgagc tcggta cccca | 1560 |
| aacgaattcg ccctttgac ggtctgcgca aaaaaacacg ttcaccttac tggcatttcg | 1620 |
| gctgagcgt tgctggctga tattcgatagc cgccttgcgt agttactgccc ggttcagggt | 1680 |
| gagcgggatt gtgtgggtgc cgcgatgcgt gaaggcacgc tggcaccggg caaacgtatt | 1740 |
| cgtccgatgc tgctgttatt aacagcgcgc gatcttggct gtgcgatcag tcacggggga | 1800 |
| ttactggatt tagcctgcgc gggtgaaatg gtgcattgcgt cctcgctgat tctggatgat | 1860 |
| atgcccgtca tggacgatgc gcagatgcgt cggggcgctc ccaccattca cacgcagttac | 1920 |
| ggtaacatg tggcgattct ggccggcggtc gctttactca gcaaagcgtt tgggtgatt | 1980 |
| gccgaggctg aaggtctgac gccgatagcc aaaactcgcg cgggtgtcgga gctgtccact | 2040 |
| gcgattggca tgcagggtct gggtcaggggc cagtttaagg acctctcgga aggcgataaaa | 2100 |
| cccccgccgcg ccgatgcccattactgtaacc aatcagttta aaaccagcac gctgtttgc | 2160 |
| gcgtcaacgc aaatggcgctc cattgcggcc aacgcgtcct gcgaagcgcgc tgagaacctg | 2220 |
| catcgtttct cgctcgatct cggccaggcc tttcagttgc ttgcgatct taccgatggc | 2280 |
| atgaccgata ccggcaaaaga catcaatcag gatgcaggta aatcaacgct ggtcaattta | 2340 |
| ttaggctcag gcgcggtcga agaacgcctg cgacagcatt tgccgttgc cagtaacac | 2400 |
| ctttccgcgg catgccaaaa cggccattcc accacccaac tttttattca ggcctgggtt | 2460 |
| gacaaaaaac tcgctgcgt cagtttaagga tgctgcattga gccattttgc ggtgatcgca | 2520 |
| ccgccccttt tcagccatgt tcgcgtctg caaaaccttgc ctcaggaatt agtggcccgc | 2580 |
| ggtcatcggttacgtttt tcagcaacat gactgcaaaag cgctggtaac gggcagcgtat | 2640 |
| atcggttcc agaccgtcgg actgcaaaacg catcccccgttgc gtcgttgcgc acaccgt | 2700 |
| cacctggccgcg cgcacccact cggaccctcg atgttacgac tgcattatgc aatggcacgt | 2760 |
| accagcgata tgctttgccg ggaactgccc gccgttttc atgcgttgc gatagagggc | 2820 |
| gtgatcggttgcg atcaaatttgcg gccggcagggt gcagtagtgc cagaagcgtc aggtctgccc | 2880 |
| tttgggttgcg tggcctgcgc gctggcgtc aaccgcgaac cgggtttgcc tctggcgttgc | 2940 |
| atgcctttcg agtacggcac cagcgatgcg gctcgaaac gctataaccac cagcgaaaaa | 3000 |
| atttatgact ggctgatgcg acgtcacat cgtgtgatgc cgcattatgc atgcagaatg | 3060 |
| ggtttagcccc cgcgtgaaaaa actgcattatc ttttttctc cactggcaca aatcagccag | 3120 |

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|---|------|
| ttgatccccg aactggattt tccccgcaaa gcgctgccag actgcttca tgcgggttggaa | 3180 |
| ccgttacggc aaccccaggg gacgcccggg tcataactt cttatccc gtcgggac | 3240 |
| aaaccccgta ttttgcctc gctgggcacc ctgcagggac atcgatggc cctgttcagg | 3300 |
| accatcgcca aagcctgcga agaggtggat ggcgcgttac tggtggcaca ctgtggcggc | 3360 |
| ctctcagcca cgcaggcagg tgaactggcc cggggcggg acattcagggt tgtggatttt | 3420 |
| gccatcaat ccgcagcact ttacaggca cagttacaa tcacacatgg tggatgaat | 3480 |
| acggtaactgg acgctattgc ttccccgaca ccgcgttacgg cgctgcccgt ggcatttgat | 3540 |
| caacctggcg tggcatcag aattgtttat catggcatcg gcaagcgtgc gtctcggtt | 3600 |
| actaccagcc atgcgctggc gcggcagatt cgatcgctgc tgactaacaac cgattacccg | 3660 |
| cagcgtatga caaaaattca ggccgcattt cgtctggcag gcggcacacc agccgccc | 3720 |
| gatattgttgc aacaggcgat gcggacactgt cagccagtac tcagtggtca ggattatgca | 3780 |
| accgcactat gatctcattt tggcgggtgc cggctggct aatggcctta tcgcgctccg | 3840 |
| gcttcagcaa cagcatccgg atatgcggat cttgcttatt gaggcgggtc ctgaggcggg | 3900 |
| agggaaaccat acctggtcct ttacgaaga ggatttaacg ctgaatcagc atcgcgttgc | 3960 |
| agcggcgtt gtggccatc actggccgcg ctaccagggtt cgtttcccc aacggcgtcg | 4020 |
| ccatgtgaac agtggctact actgcgtgac ctcccgcat ttgcgggaa tactccggca | 4080 |
| acagtttggaa caacatttgc ggctgcatac cgcgggttca gccgttcatg ctgaatcggt | 4140 |
| ccagtttagcg gatggccggaa ttattcatgc cagtagtgc atcgacggac ggggttacac | 4200 |
| gcctgattct gcactacgcg taggattcca ggcatttac ggtcaggagt ggcaactgag | 4260 |
| cgcggccat ggttatcgat caccgattat catggatgcg acggcgtatc agcaaatgg | 4320 |
| ctaccgcttt gtttataccc tgccgctttc cgcaaccgca ctgctgatgc aagacacaca | 4380 |
| ctacattgac aaggctaattt ttcaaggccgaa acggggcggtt cagaacatttgc gcgattatgc | 4440 |
| tgcgcgacag ggttggccgt tacagacgtt gctgcgggaa gaacagggtt cattgccc | 4500 |
| tacgttaacg ggcgataatc gtcagttttt gcaacagcaa cgcgaagcct gtagcggatt | 4560 |
| acgcgcccggg ctgtttcatc cgacaaccgg ctactcccta ccgcgtcggtt tggcgtggc | 4620 |
| cgatcgcttc agcgcgttgc atgtgtttac ctcttcctct gttcaccaga cgattgctca | 4680 |
| ctttgcccag caacgttggc agcaacagggtt gttttccgc atgctgaatc gcatgttgc | 4740 |
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| tgc | 3423 |